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Amendments to the Specification:

Please replace the paragraph beginning on page 9, beginning at line 20, with the following amended paragraph:

Figure 8. Figures 8a and 8b. Multiple alignment of maize sucrose synthase amino acid sequences.

Please replace the paragraph beginning on page 9, beginning at line 23, with the following amended paragraph:

Figure 9. Figures 9a - 9f. Multiple alignment of maize sucrose synthase polynucleotides.

Please replace the paragraph beginning on page 71, beginning at line 24, with the following amended paragraph:

4. A Sal-A20 oligo nucleotide of SEQ ID NO 3:NO: 3 TCG ACC CAC GCG TCC GAA AAA AAA AAA AAA AAA AAA, removes clones containing a poly A tail but no cDNA.

Please replace the paragraph beginning on page 72, beginning at line 7, with the following amended paragraph:

Gene identities can be determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) J. Mol. Biol. 215:403-410; see also the World Wide Web at www. ncbi.nlm.nih.gov/BLAST/) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from

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the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of
the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The
cDNA sequences are analyzed for similarity to all publicly available DNA sequences
contained in the "nr" database using the BLASTN algorithm. The DNA sequences
are translated in all reading frames and compared for similarity to all publicly
available protein sequences contained in the "nr" database using the BLASTX
algorithm (Gish, W. and States, D. J. *Nature Genetics 3*:266-272 (1993)) provided
by the NCBI. In some cases, the sequencing data from two or more clones
containing overlapping segments of DNA are used to construct contiguous DNA
sequences.